

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended) A method for multiplex detection of methylation in methylated target sequences ~~on target nucleic acids~~ comprising:
 - (a) providing a first population of double-stranded target nucleic acids labeled with a purification tag, wherein said target nucleic acids comprise potentially methylated target sequences;
 - (b) cleaving said first population of target nucleic acids with an enzyme,

whereby said enzyme selectively cleaves at [[said]] unmethylated target sequences ~~that are unmethylated~~, forming a second population of cleaved target nucleic acids sequences labeled with a purification tag,

with the proviso that said enzyme does not cleave at [[said]] methylated target sequences thereby providing non-cleaved target nucleic acids ~~that are methylated~~;
 - (c) immobilizing at least non-cleaved ~~said~~ target nucleic acids by said purification tag;
and
 - (d) detecting the presence of said ~~first population comprising~~ non-cleaved target nucleic acids, [[acid]] wherein said detecting comprises:
 - (i) contacting said immobilized non-cleaved target nucleic acids with a composition comprising a plurality of target probes, thereby selectively forming a plurality of hybridization complexes between said immobilized non-cleaved target nucleic acids and said target probes, said probes comprising:

a first region complementary to a first region of a non-cleaved target nucleic acid and a second region comprising a detection sequence complementary to a potentially methylated target sequence,

whereby the presence of said hybridization complexes ~~first population comprising non-cleaved target nucleic acid~~ indicates the presence of methylation in said target sequences ~~methylated target nucleic acids~~.

2. (Previously presented) The method according to claim 1, wherein said purification tag comprises biotin.

3. (Previously presented) The method according to claim 1, wherein said enzyme is HpaII.

4. (Canceled).

5. (Currently amended) A method for multiplex detection of methylation in target sequences comprising:

(a) providing a first population of double-stranded target nucleic acids labeled with a purification tag, wherein said target nucleic acids comprise potentially methylated target sequences;

(b) cleaving said first population of target nucleic acids with an enzyme,

whereby said enzyme selectively cleaves at unmethylated target sequences, forming a second population of cleaved target acids labeled with a purification tag,

with the proviso that said enzyme does not cleave at methylated target sequences thereby providing non-cleaved target nucleic acids;

(c) immobilizing at least non-cleaved target nucleic acids by said purification tag; and

(d) detecting the presence of said non-cleaved target nucleic acids wherein said detecting comprises:

(i) contacting said immobilized non-cleaved target nucleic acids with a composition comprising a plurality of target probes, thereby selectively forming a plurality of hybridization complexes between said immobilized non-cleaved target nucleic acids and said target probes, said probes comprising:

a region complementary to a region of a non-cleaved target nucleic acid and ~~The method according to claim 4, wherein said probes further comprise at least a first universal priming sequence and step (f) further comprises:~~

(ii)[(i)] contacting said hybridization complexes with a composition comprising:

- a) at least first universal primers;
- b) dNTPs; and
- c) polymerase,

whereby said probes are amplified to form a plurality of amplicons containing said target sequences; and

(ii) detecting said amplicons,

whereby the presence of said amplicons is [[as]] an indication of the presence of methylation in said target sequences ~~methylated target sequence.~~

Claims 6-30 (Canceled).

31. (New) The method according to claim 5, wherein said purification tag comprises biotin.

32. (New) The method according to claim 5, wherein said enzyme is HpaII.